

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SOPPET, DANIEL R.
RUBEN, STEVEN M.
- (ii) TITLE OF INVENTION: HEMATOPOIETIC SIGNALING FACTOR
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: US
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/035,577
 - (B) FILING DATE: 16-JAN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0600001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 66..1202
- (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 144..1202

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 66..141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGGCTTCGG GTCGGTGCAA GGCAGGCGCA CGGGGAAGGG CGCGCCGCGC GGCCGCCACC	60
CCACC ATG CTC AAG CGC TGC GGC CGG CGC CTG CTG CTG GCG CTG GCG	107
Met Leu Lys Arg Cys Gly Arg Arg Leu Leu Leu Ala Leu Ala	
-26 -25 -20 -15	
GGC GCG CTG CTC GCC TGC CTG CTG GTG CTC ACC GCC GAC CCG CCG CCG	155
Gly Ala Leu Leu Ala Cys Leu Leu Val Leu Thr Ala Asp Pro Pro Pro	
-10 -5 1	
CCT CCA CTG CCC GCC GAG CGC GGC CGG CGC GCG CTG CGC AGC CTG GCG	203
Pro Pro Leu Pro Ala Glu Arg Gly Arg Arg Ala Leu Arg Ser Leu Ala	
5 10 15 20	
GGC CCC GCG GGG GCT GCC CCG GCG CCC GGG CTG GGG GCG GCG GCG GCG	251
Gly Pro Ala Gly Ala Ala Pro Ala Pro Gly Leu Gly Ala Ala Ala Ala	
25 30 35	
GCG CCC GGG GCG CTG GTC CGC GAC GTG CAC AGT CTG TCC GAG TAC TTC	299
Ala Pro Gly Ala Leu Val Arg Asp Val His Ser Leu Ser Glu Tyr Phe	
40 45 50	
AGC CTG CTC ACC CGC GCG CGC AGA GAT GCG GGC CCG CCG CCC GGG GCT	347
Ser Leu Leu Thr Arg Ala Arg Arg Asp Ala Gly Pro Pro Pro Gly Ala	
55 60 65	
GCC CCC CGC CCC GCC GAC GGC CAC CCG CGC CCC CTG GCC GAG CCG CTC	395
Ala Pro Arg Pro Ala Asp Gly His Pro Arg Pro Leu Ala Glu Pro Leu	
70 75 80	
GCG CCC CGA GAC GTC TTC ATC GCT GTC AAG ACC ACC AAA AAG TTC CAC	443
Ala Pro Arg Asp Val Phe Ile Ala Val Lys Thr Thr Lys Lys Phe His	
85 90 95 100	
CGC GCG CGC CTC GAC CTG CTG CTG GAG ACC TGG ATC TCG CGC CAC AAG	491
Arg Ala Arg Leu Asp Leu Leu Leu Glu Thr Trp Ile Ser Arg His Lys	
105 110 115	
GAG ATG ACG TTC ATC TTC ACT GAC GGG GAA GAT GAG GCC CTG GCC AGG	539
Glu Met Thr Phe Ile Phe Thr Asp Gly Glu Asp Glu Ala Leu Ala Arg	
120 125 130	
CAC ACG GGC AAC GTG GTC ATC ACA AAC TGC TCG GCC GCC CAC AGC CGC	587
His Thr Gly Asn Val Val Ile Thr Asn Cys Ser Ala Ala His Ser Arg	
135 140 145	
CAG GCG CTG TCC TGC AAG ATG GCC GTG GAG TAT GAC CGC TTC ATC GAG	635
Gln Ala Leu Ser Cys Lys Met Ala Val Glu Tyr Asp Arg Phe Ile Glu	
150 155 160	

TCC GGC AGG AAG TGG TTC TGC CAC GTG GAC GAT GAC AAC TAC GTC AAC	683
Ser Gly Arg Lys Trp Phe Cys His Val Asp Asp Asp Asn Tyr Val Asn	
165 170 175 180	
CTG CGG ACC CTG CTG CGA CTG CTG GCC AGC TAC CCG CAC ACG CGG GAC	731
Leu Arg Thr Leu Leu Arg Leu Leu Ala Ser Tyr Pro His Thr Arg Asp	
185 190 195	
GTC TAC GTC GGC AAG CCC AGC CTG GAC AGG CCC ATC CAG GCC ATG GAG	779
Val Tyr Val Gly Lys Pro Ser Leu Asp Arg Pro Ile Gln Ala Met Glu	
200 205 210	
CGG GTC AGC GAG AAC AAG GTG CGT CCT GTC CAC TTC TGG TTT GCC ACG	827
Arg Val Ser Glu Asn Lys Val Arg Pro Val His Phe Trp Phe Ala Thr	
215 220 225	
GGC GGC GCT GGC TTC TGC ATC AGC CGT GGG CTG GCT CTG AAG ATG AGC	875
Gly Gly Ala Gly Phe Cys Ile Ser Arg Gly Leu Ala Leu Lys Met Ser	
230 235 240	
CCG TGG GCC AGC GGG GGT CAC TTC ATG AAT ACG GCT GAG CGG ATC CGG	923
Pro Trp Ala Ser Gly Gly His Phe Met Asn Thr Ala Glu Arg Ile Arg	
245 250 255 260	
CTG CCT GAT GAC TGC ACC ATC GGC TAC ATC GTG GAG GCC CTG CTG GGT	971
Leu Pro Asp Asp Cys Thr Ile Gly Tyr Ile Val Glu Ala Leu Leu Gly	
265 270 275	
GTG CCC CTC ATC CGC AGC GGC CTC TTC CAC TCC CAC CTG GAG AAC CTG	1019
Val Pro Leu Ile Arg Ser Gly Leu Phe His Ser His Leu Glu Asn Leu	
280 285 290	
CAG CAG GTG CCC ACC TCG GAG CTC CAC GAG CAG GTG ACG CTG AGC TAC	1067
Gln Gln Val Pro Thr Ser Glu Leu His Glu Gln Val Thr Leu Ser Tyr	
295 300 305	
GGT ATG TTT GAA AAC AAG CGG AAC GCC GTC CAC GTG AAG GGG CCC TTC	1115
Gly Met Phe Glu Asn Lys Arg Asn Ala Val His Val Lys Gly Pro Phe	
310 315 320	
TCG GTG GAG GCC GAC CCA TCC AGG TTC CGC TCC ATC CAC TGC CAC CTG	1163
Ser Val Glu Ala Asp Pro Ser Arg Phe Arg Ser Ile His Cys His Leu	
325 330 335 340	
TAC CCG GAC ACA CCC TGG TGT CCC CGC ACT GCC ATC TTC TAGTGGCCAT	1212
Tyr Pro Asp Thr Pro Trp Cys Pro Arg Thr Ala Ile Phe	
345 350	
GGCTGAGACC CAATCCCTGG GCGCCCCTGG TATCCAAAGG GCCCAGGGAC CCTGTTGCGC	1272
TGCCCTGGCC TCGGCATTCTG AGGCTCCCCCT AGGGCCGTGC CTGTGCGTGT GCGTGTGCGT	1332
GTGTGTGTGT GTGTACTGCA TGCCACCCG GGTAGCAGGC TGCTGGGCAG TTCTGCTCTG	1392
TGGAGGGGCG GGCACCAGCG CCACTTATGT GCCTCTGCTC CGAGGGCCAG TGGTATGGAG	1452
GGTCTGCTTG GAGGAAGGAT TTGTGTGTCTG GAGGACACTC CGAGGGCAAT TCTGTTAGGA	1512
TTTGTGGATC TTTCTACAGC TACGGGGCTC CGG	1545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Leu Lys Arg Cys Gly Arg Arg Leu Leu Leu Ala Leu Ala Gly Ala
-26 -25                               -20                -15

Leu Leu Ala Cys Leu Leu Val Leu Thr Ala Asp Pro Pro Pro Pro Pro
-10                               -5                        1      5

Leu Pro Ala Glu Arg Gly Arg Arg Ala Leu Arg Ser Leu Ala Gly Pro
      10                        15                20

Ala Gly Ala Ala Pro Ala Pro Gly Leu Gly Ala Ala Ala Ala Ala Pro
      25                        30                35

Gly Ala Leu Val Arg Asp Val His Ser Leu Ser Glu Tyr Phe Ser Leu
      40                        45                50

Leu Thr Arg Ala Arg Arg Asp Ala Gly Pro Pro Pro Gly Ala Ala Pro
      55                        60                65                70

Arg Pro Ala Asp Gly His Pro Arg Pro Leu Ala Glu Pro Leu Ala Pro
      75                        80                85

Arg Asp Val Phe Ile Ala Val Lys Thr Thr Lys Lys Phe His Arg Ala
      90                        95                100

Arg Leu Asp Leu Leu Leu Glu Thr Trp Ile Ser Arg His Lys Glu Met
      105                       110                115

Thr Phe Ile Phe Thr Asp Gly Glu Asp Glu Ala Leu Ala Arg His Thr
      120                       125                130

Gly Asn Val Val Ile Thr Asn Cys Ser Ala Ala His Ser Arg Gln Ala
      135                       140                145                150

Leu Ser Cys Lys Met Ala Val Glu Tyr Asp Arg Phe Ile Glu Ser Gly
      155                       160                165

Arg Lys Trp Phe Cys His Val Asp Asp Asp Asn Tyr Val Asn Leu Arg
      170                       175                180

Thr Leu Leu Arg Leu Leu Ala Ser Tyr Pro His Thr Arg Asp Val Tyr
      185                       190                195

Val Gly Lys Pro Ser Leu Asp Arg Pro Ile Gln Ala Met Glu Arg Val
      200                       205                210

Ser Glu Asn Lys Val Arg Pro Val His Phe Trp Phe Ala Thr Gly Gly
      215                       220                225                230

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Ala	Gly	Phe	Cys	Ile	Ser	Arg	Gly	Leu	Ala	Leu	Lys	Met	Ser	Pro	Trp
				235					240					245	
Ala	Ser	Gly	Gly	His	Phe	Met	Asn	Thr	Ala	Glu	Arg	Ile	Arg	Leu	Pro
			250					255					260		
Asp	Asp	Cys	Thr	Ile	Gly	Tyr	Ile	Val	Glu	Ala	Leu	Leu	Gly	Val	Pro
		265					270					275			
Leu	Ile	Arg	Ser	Gly	Leu	Phe	His	Ser	His	Leu	Glu	Asn	Leu	Gln	Gln
	280					285					290				
Val	Pro	Thr	Ser	Glu	Leu	His	Glu	Gln	Val	Thr	Leu	Ser	Tyr	Gly	Met
295					300					305					310
Phe	Glu	Asn	Lys	Arg	Asn	Ala	Val	His	Val	Lys	Gly	Pro	Phe	Ser	Val
				315					320					325	
Glu	Ala	Asp	Pro	Ser	Arg	Phe	Arg	Ser	Ile	His	Cys	His	Leu	Tyr	Pro
			330					335					340		
Asp	Thr	Pro	Trp	Cys	Pro	Arg	Thr	Ala	Ile	Phe					
		345					350								

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	Lys	Asn	Trp	Gly	Lys	Lys	Leu	Leu	Leu	Ser	Ile	Val	Gly	Ala
1				5					10					15	
Thr	Leu	Thr	Cys	Leu	Leu	Val	Leu	Val	Val	Asp	Gln	Gln	Ser	Arg	His
			20					25					30		
Met	Leu	Glu	Thr	Gln	Ser	Asp	His	Glu	Pro	Gly	Ser	Ala	Ala	Ala	Val
		35					40					45			
His	Leu	Arg	Ala	Asp	Leu	Asp	Pro	Ala	Asn	Pro	Gly	Asp	Gly	Gly	Asp
	50					55					60				
Pro	Ala	Asn	Ser	Ala	Gln	Asp	Ser	Gly	Thr	Phe	Ser	Ala	Tyr	Phe	Asn
65					70				75						80
Lys	Leu	Thr	Arg	Val	Arg	Arg	Asp	Val	Glu	Gln	Val	Ala	Ala	Pro	Ser
			85						90					95	
Lys	Asp	Ser	Ala	Ala	Pro	Glu	Glu	Asp	Ile	Thr	Ala	Asn	Asp	Val	Phe
			100					105					110		

Ile	Ala	Val	Lys	Thr	Thr	Lys	Lys	Phe	His	Arg	Ser	Arg	Met	Asp	Leu	115	120	125
Leu	Met	Asp	Thr	Trp	Ile	Ser	Arg	Asn	Lys	Glu	Gln	Thr	Phe	Ile	Phe	130	135	140
Thr	Asp	Gly	Glu	Asp	Glu	Glu	Leu	Gln	Lys	Lys	Thr	Gly	Asn	Val	Glu	145	150	155
Ser	Thr	Asn	Cys	Ser	Ala	Ala	His	Ser	Arg	Gln	Ala	Leu	Ser	Cys	Lys	165	170	175
Met	Ala	Val	Glu	Tyr	Asp	Lys	Phe	Ile	Glu	Ser	Asp	Lys	Lys	Trp	Phe	180	185	190
Cys	His	Val	Asp	Asp	Asp	Asn	Tyr	Val	Asn	Val	Arg	Thr	Leu	Val	Lys	195	200	205
Leu	Leu	Ser	Arg	Tyr	Ser	His	Thr	Asn	Asp	Ile	Tyr	Ile	Gly	Lys	Pro	210	215	220
Ser	Leu	Asp	Arg	Pro	Ile	Gln	Ala	Thr	Glu	Arg	Ile	Ser	Glu	Ser	Asn	225	230	235
Met	Arg	Pro	Val	Asn	Phe	Trp	Phe	Ala	Thr	Gly	Gly	Ala	Gly	Phe	Cys	245	250	255
Ile	Ser	Arg	Gly	Leu	Ala	Leu	Lys	Met	Ser	Pro	Trp	Ala	Ser	Gly	Gly	260	265	270
His	Phe	Met	Asn	Thr	Ala	Glu	Lys	Ile	Arg	Leu	Pro	Asp	Asp	Cys	Thr	275	280	285
Ile	Gly	Tyr	Ile	Ile	Glu	Ser	Val	Leu	Gly	Val	Lys	Leu	Ile	Arg	Ser	290	295	300
Asn	Leu	Phe	His	Ser	His	Leu	Glu	Asn	Leu	His	Gln	Val	Pro	Gln	Ser	305	310	315
Glu	Ile	His	Asn	Gln	Val	Thr	Leu	Ser	Tyr	Gly	Met	Phe	Glu	Asn	Lys	325	330	335
Arg	Asn	Ala	Ile	Leu	Met	Lys	Gly	Ala	Phe	Ser	Val	Glu	Glu	Asp	Pro	340	345	350
Ser	Arg	Phe	Arg	Ser	Val	His	Cys	Leu	Leu	Tyr	Pro	Asp	Thr	Pro	Trp	355	360	365
Cys	Pro	Trp	Lys	Ala	Ala	Tyr										370	375	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
- CACCGTCGAC CCGCCGCCGC CTCCACTGC 29
- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- GGTCTAAGCT TTGGCCATTA GAAGATGGCA GTGCGGG 37
- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
- GCGTCTAGAC CGCCATCATG CTCAAGCGCT GCGG 34
- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
- GTAATACGAC TCACTATAGG GC 22
- (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGTCTAGACG CGGCCGCCAC CCCACCATGC TC

32

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGGGTCTAGA CCATGGCCAC TAGAAGATG

29

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGGTCTAGA CCATGGCCAC TAAGCGTAGT CTGGGACGTC GTATGGGTAG AAGATG

56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGTTTGCNA CGGGNGGCGC TGGCTTCTNC ATCANCCGTG GGCTGGCTCT AAAGATGAGC	60
CCGTGGGCCA GCGGGGGTNA CTTTCATGAAT ACGGCTGAGC GGATCCGGCN GCCTGATGAC	120
TGCACCATCG GCTACATCGT GGAGGCCCTG CTGGGTGTGC CCCTNATCCG CAGCGGCCTN	180
TTCCACTCCC ACCTGGAGAA CCTGCAGCAG GTGCCCACCT CGGAGCTCCA CGGAGCAGGT	240
NACGCTGAGC TTACGGTATT TTTTGAAAAA AAGCGGGAAC GCCGTTCAC GTNAAAGGGG	300
GCCTTTTTTN GGTGGGAGG GCCGACCCAT TCCAGGTTTC CGTTTNCATT CCANTTGCCA	360
ACTTTTAACC NGGGAAAAAA CCTTGGTNTT TCCCCGAAAT TGNAATTTTT TAGGTTGG	418

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCACGAGTG AAGGGCTGCC TGCTGAAGGC CGATTTTCTC CTTCCAGACG TTCATCTTCA	60
CTGACGGGGA AGATGAGGCC CTGGCCAGGC ACACGGGTGA GCCCTGGACT TGGGGCGGGA	120
NGGGGCCCAA GCCTCCATCC AGAGCCGAAC GCTCCCCCTC CAGTCTCCCT GCCCCTCTGG	180
GCCGAGAAGT CACCAAGGGC AGGACANGGA GGGCAGTTTA CTCATGGGGT TTGCTCCATG	240
CCCCGGCCCA AACTCGGGN CCCCCAATTC TCATGCAAAT GAAGCCCATT CAGCCCCCG	300
GGTTCCTTTG AGCCAAGCAG CGGCAAAAGT GCGGTTCTG GNAAAAGTGC TGATTGGCGG	360
GGCGGGGCGC CTTGAAGGGT TGGTTCGGA GTCAAAGCCA AGCCCGAGTA AGTTGGGAGT	420
ANGCGCCGGC CAGTTAANAA GGG	443

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCGAGTCCG GGTGCAGGTG GCAATGGACA GAGCGGAACC TGGATGGGTC AGCTTCCACA	60
GAGAATGGTC CCTTGATGTG CACTGCGTTC CGCTTGTTCT CAAACATGCC ATAGCTCAGG	120
GTCACCTGCT CATGAAGCTC GGTGGTGGGC ACCTGCTGCA GGTTCTCTAG GTGGGAGTGG	180
AAGAGGCCGC TCCGGATGAG GGGTACACCC AGCAGAGCCT CTACAATGTA GCCAATGGTG	240
CAGTCATCGG GGAGCCGGAT GCGCTCTGCC GTGCTCATGA AGTGTCTCTCC ACTGGCCCAT	300
GGGCCATCTT TAGGGCCAGC CCTCGGCTGA TGCAGAAGCC AGCTCCTCCG GTGGCAAACC	360
AAAAGTGGAC AGGTCTCACT TTGTGCTCGC TGATCCGTTC TGTGGCCTGG ATGGGCCTGT	420
CCAGGCTGGG CTTGCGATGT ACACGTCTTG GGTGTGGGGA TAGCTGGCCA GGAAGCGCAG	480
CAGCGCCCGG AAGTTGACGT AGTTGTCATC ATC	513

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGCCCCCTG GCCGAGCCGC TNCGCGCCCC GAGACGTCTT CATCGCTGTC AAGACCACCA	60
AAAAGTTCCA CCGCGCGCGC CTCGACCTGC TGCTGGAGAC CTGGATCTCG CGCCACAAGG	120
AGATGACGTT CATCTTCACT GACGGGGAAG ATGAGGCCCT GGCAGGCACA CGGGCAACGT	180
GGTCATCACA AACTGCTCGG CCGCCACAG CCGCCAGCTT GNTTCCTGCA AGATGGCCGT	240
GGAGTATGAC CGCTTCATCG AGTCCGGCAG AAGTGGTTCT GCCACGTGGA CGATGACAAC	300
TACGTCAACC TCGGGGCCCT GCTNCGGCTG CTGGCCAGCT GACCCGCACA CG	352

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACAGGTCTCA	CTTTGTGCTC	GCTGATCCGT	TCTGTGGCCT	GGATGGGCTG	TCCAGCTGGG	60
CTTGCGATGT	CACGTCTTGG	GTGTGGGGAT	AGCTGGCCAG	GAGCCGCAGC	AGCGCCCGGA	120
GTTGACGTAG	TTGTCATCAT	CCACGTGGCA	GAACCACTTC	TTCCCAGACT	CAATGAATCG	180
GTCATACTCC	ACAGCCATCT	TGCAGGACAG	AGCCTGGCGC	TGTGGGCCGA	GGAGCAGTTG	240
GTGAGCACCA	CATTGCCTGT	GAGCTTGGCC	AGAGCTTCGT	CCTCCCCATC	AGTGAAGATG	300
AACGTCATCT	CCTTGTGGCG	CGAGATCCAG	GTCTCGAACA	GCAGATCGAG	CCGCGCGCGG	360
TGAAACTTTC	TGGTGGTCTT	GACGGCGATG	AAGACGTCGC	GAGGGGACAG	AACTTTCGGC	420
GGGGGACGCG	GATGGGCGTC	GCCCTGCGA				449